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<120> BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
DELIVERY

<140> As yet unassigned

<150> 60/213,653

<151> 2000-06-23

<160> 45

<170> PatentIn Ver. / 2.0

$\langle 210 \rangle$ 1

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<213> Homo sapiens

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Lys Ala Pro Lys Ser Pro Ala Lys Ala Lys
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Understanding the role of the various components of the system is essential for effective management. The following table provides a summary of the key elements and their functions:

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2025年12月

5

<213> Homo sapiens

5.

<213> Homo sapiens

5

<213> Homo sapiens

15

20

<213> Simian virus 40

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[illegible]

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sFv')

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      20             25             30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
      35             40             45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
      50             55             60
```

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chimeric single chain binding polypeptide (C6ML3-9
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sFv')

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Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
                35                      40                     45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
                50                      55                     60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
                65                      70                     75                     80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
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      chimeric single chain binding polypeptide
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THE UNIVERSITY OF CHICAGO

<211> 287

<213> Artificial Sequence

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Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
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Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp
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Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser

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Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Glu Lys Asp Glu Leu
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ccggggaaag	gcctggagta	catggggctc	atctatcctg	gtgactctga	caccaaatac	180
aqccqtcct	tccaaqqcca	ggtcaccatc	tcagtcgaca	agtcgcgcag	cactgcctac	240

1. *Chlorophyll a* (Chl *a*) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum. Chl *a* is essential for the light-dependent reactions of photosynthesis, where it converts light energy into chemical energy.

2. *Chlorophyll b* (Chl *b*) is an accessory pigment found in green plants and algae. It absorbs light energy in the blue and orange-red regions of the visible spectrum. Chl *b* transfers the absorbed energy to Chl *a* for use in photosynthesis.

3. *Carotenoids* are a group of pigments that include carotenes and xanthophylls. They absorb light energy in the blue and green regions of the visible spectrum. Carotenoids transfer energy to Chl *a* and also play a role in protecting the photosynthetic apparatus from damage by excess light energy.

4. *Xanthophylls* are a subclass of carotenoids that include pigments like lutein and zeaxanthin. They absorb light energy in the blue and green regions of the visible spectrum and transfer energy to Chl *a*. Xanthophylls are also involved in the xanthophyll cycle, which helps regulate light absorption and protect the photosynthetic apparatus.

5. *Anthocyanins* are water-soluble pigments that give plants red, purple, and blue colors. They are not directly involved in photosynthesis but can protect plants from damage by absorbing excess light energy and acting as antioxidants.

```

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Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
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Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
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Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
      65                   70                   75                   80

```

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Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
      85                   90                   95

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Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp
      100                   105                   110

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```

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
      115                   120                   125

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Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

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130		135		140
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln				
145		150		155 160
Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn				
	165		170	175
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu				
	180		185	190
Ile Tyr Asp His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser				
	195		200	205
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg				
	210		215	220
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Tyr Thr Leu				
	225		230	235 240
Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala				
	245		250	255
Ala Ala His His His His His His Gly Gly Gly Gly Cys Leu Glu Ser				
	260		265	270
Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser Lys Lys Ser Ala Lys Lys				
	275		280	285
Thr Pro Lys Lys Ala Lys Lys Pro				
	290		295	

<210> 43

<211> 888

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human/murine
chimeric single chain binding polypeptide
(C6ML3-9sFv'-L2-H14)

<400> 43

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cccgggaaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac 180
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09080724.000001

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cagggcaccc tggtcaccgt ctctcaggt ggaggcgggt caggcggagg tggctctggc 420
ggtggcggat cgcagtctgt gttgacgcag ccgccctcag tgtctgcggc cccaggacag 480
aaggtcacca tctcctgctc tggaagcagc tccaacattg ggaataatta tgtatcctgg 540
taccagcagc tcccaggaac agccccaaa ctctcatct atgatcacac caatcgcccc 600
gcaggggtcc ctgaccgatt ctctggctcc aagtctggca cctcagcctc cctggccatc 660
agtgggttcc ggtccgagga tgaggctgat tattactgtg cctcctggga ctacaccctc 720
tcgggctggg tggtcggcgg aggaaccaag ctgaccgtcc taggtgcggc cgcacaccat 780
catcaccatc acggtggtgg cggctgcctc gagtctagca gctccggttc ctctagctct 840
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<210> 44

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human/murine
chimeric single chain binding polypeptide
(C6ML3-9sFv'-L2-nls)

<400> 44

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
  1                   5                   10                   15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
      20                   25                   30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
      35                   40                   45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
      50                   55                   60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
      65                   70                   75                   80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
      85                   90                   95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp
      100                   105                   110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
      115                   120                   125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

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000001.000001

caggtgcagc	tggtgcagtc	tggggcagag	gtgaaaaagc	cgggggagtc	tctgaagatc	60
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ccgggaaag	gcctggagta	catggggctc	atctatcctg	gtgactctga	caccaaatac	180
agcccgctct	tccaaggcca	ggtcaccatc	tcagtcgaca	agtccgtcag	cactgcctac	240

ttgcaatgga	gcagttctgaa	gccctcggac	agcgccgtgt	atttttgtgc	gagacatgac	300
gtgggatatt	gcagtagttc	caactgcgca	aagtggcctg	aatacttcca	gcattggggc	360
cagggcaccc	tggtcacctg	ctcctcaggt	ggaggcggtt	caggcgagg	tggtctctggc	420
ggtggcggat	cgcagtctgt	gttgacgcag	ccgccctcag	tgtctgcggc	cccaggacag	480
aaggtcacca	tctcctgctc	tggaaagcagc	tccaacattg	ggaataatta	tgtatcctgg	540
taccagcagc	tcccaggaac	agcccccaaa	ctcctcatct	atgatcacac	caatcggcc	600
gcaggggtcc	ctgaccgatt	ctctggctcc	aagtctggca	cctcagcctc	cctggccatc	660
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tcgggctggg	tgttcggcgg	aggaaccaag	ctgaccgtcc	taggtgcggc	cgcacaccat	780
catcaccatc	acggtggtgg	cggctgcctc	gagtctagca	gctccgggtc	ctctagctct	840
ggatccactc	cgccgaaaaa	gaaacgtaaa	gtg			873

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